OSIRIS Release Notes Version 2.11.1

Version 2.11.1 is a bug fix version

Version 2.11.1 fixes two bugs that could occur under rare conditions.

Bug Fixes

Pull-up analysis bug.
Fixed an uncommon bug that in extremely rare circumstances could result in an allele that comigrates with a peak in another channel being called a pull-up in circumstances where the "Min RFU for a peak to be considered as a peak that causes pull-up" in the Sample Limits tab of the Lab Settings is set too high.

ILS peaks with no label.
Fixed a bug in which ILS peaks that were also called as pull-up were not given a base pair label. While this produced no analysis errors, it could result in display issues.

Version 2.11 Release notes

Improvements in OSIRIS Version 2.11

Version 2.11. includes substantial improvements over previous versions

New Features

Improved Display
- OSIRIS now allows users to display either Time or Bases on the x-axis of the Graph view.

Improved Artifact Analysis
- Allele-specific stutter analysis has been added as an option. Allowing the stutter threshold to increase with increasing allele size gives more accurate discrimination between alleles and stutter. Users can set their own threshold levels.
- Allele peak heights corrected for coincident pull-up signal can be used in stutter and adenylation analysis when determining whether a peak falls under a threshold, to make discrimination between alleles and artifacts more accurate.
- Improved pull-up analysis by including low-level raw data peaks below analytical threshold in the overall pull-up pattern analysis, resulting in better identification of very low level pull-up peaks.
- Added settings to reduce the possibility of extraneous "excessive residual displacement" artifact calls.

Improved Baseline and Peak Analysis
- Added options for improved peak curve fitting at the base of large peaks, which can also improve the analysis of low level shoulder peaks.
- Improved baseline estimation at the edges of peaks.

Process Quality Control Metrics
- Multiple metrics have been added that can be exported for quality control of the DNA analysis process. This includes data regarding the performance of the genetic analyzer and sample extraction/amplification to allow predictive monitoring for issues like poor spectral color separation matrix, capillary failure, and extraction/amplification problems.

Improved Editing
- <u>Reduced editing</u> due to artifacts in ILS and ladders. Many minor artifacts do not impact the spacing, accuracy and validity of ILS and ladder profiles, but previously required editing. Options have been added allowing users to specify that artifacts that do not impact ILS or ladder validity be non-critical and not require editing. These artifacts are still called and displayed for review.
- <u>Added options to allow editing of "restricted priority" peaks</u> and peaks that are below analytical threshold (and above detection threshold).

Improved Network Administration
- Implemented shared Lab Settings and Export settings in a network environment where both Windows and Macintosh versions of OSIRIS are in use.
- Improved the management of user permissions for Lab Settings and Exports.

Improved CODIS CMF file exports: Can include comments in the Sample Comments field of the Plate Template in the ABI Genetic Analyzer Data Collection Software that OSIRIS can export to the CODIS CMF Comment field.

Improved ladder analysis: Improved robustness of bi-allelic loci, such as Amelogenin. Reduces artifacts.

New Kit /Lab Settings

Added example Lab Settings for Sole Source and Mixed samples
PowerPlex Fusion HID Sole Source and *GlobalFiler HIG Mixture* lab default settings include all of OSIRIS novel features and updates and can serve as a starting point for laboratories to optimize their settings for sole source and potential mixed samples. Both can be modified for use with .fsa files, and the settings can be copied to other kits. Both will need to be modified for lab's own analytical thresholds and desired peak sensitivity.

Bug Fixes

Pull-up analysis bug.
Fixed an uncommon bug that in extremely rare circumstances could result in an allele that comigrates with a peak in another channel being called a pull-up. This bug was fixed by making better use of peaks that did not comigrate with a peak in the pull-up channel, or that comigrate with raw data above the noise level for the channel.

ILS peaks with no label.
Fixed a bug in which ILS peaks that were also called as pull-up were not given a base pair label. While this produced no analysis errors, it could result in display issues.

Fixed minor bugs that did not impact accuracy.